

**IN THE CLAIMS:**

Please amend claims 1, 11 and 16 as follows:

1. (Presently Amended) An isolated rpoB nucleic acid molecule consisting of [at least] **from** about 100 contiguous bases **to about all** of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9 and 10.

2. (Previously Amended) An isolated nucleic acid molecule consisting of a rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9 and 10.

3. (Previously Amended) A probe which is the complement of a rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.

4. (Previously Amended) A method of classifying a mycobacteria, comprising providing a sample comprising a mycobacterial rpoB target nucleic acid from a mycobacteria;

determining the sequence of a segment of at least 50 contiguous bases from the target nucleic acid;

comparing the determined sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10; and

classifying the mycobacteria from the extent of similarity of the compared sequences.

5. (Original) The method of claim 4, wherein at least 100 contiguous bases are determined from the target nucleic acid.

6. (Previously Amended) The method of claim 4, wherein the determined sequence is compared with at least nine sequences selected from the group consisting SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.

7. (Previously Amended) A method of classifying a mycobacteria, comprising providing a sample comprising a mycobacterial rpoB target nucleic acid;

determining the identity of one or more bases in the target sequence at one or more positions corresponding to one or more bases in a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10, wherein the one or more bases of the sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10 differ from the corresponding one or more bases in SEQ ID NO. 1 when the sequences are maximally aligned, the identity of the one or more bases characterizing the species of mycobacteria that is present in the sample;

comparing the identified one or more bases in the target sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10; and

classifying the mycobacteria from the extent of similarity between the one or more bases identified in the target sequence and the corresponding one or more bases in the compared sequences.

8. (Previously Amended) The method of claim 7, wherein the identity of at least 10 bases in the target nucleic acid at positions corresponding to the one or more bases in the sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10 is determined.

9. (Previously Amended) The method of claim 8, wherein the identity of at least 20 bases in the target sequence at positions corresponding to the one or more bases in the sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10 is determined.

10. (Previously Amended) The method of claim 9, further comprising comparing the at least 20 determined bases with at least 20 bases occupying corresponding positions in each of at least nine sequences selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.

11. (Presently Amended) A polynucleotide probe or primer that **is fully complementary to and** hybridizes under stringent hybridization conditions to at least a contiguous segment of a mycobacterial rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 or its complement without hybridizing to the *M.*

*tuberculosis* sequence of SEQ ID NO: 1 or its complement, wherein the contiguous segment of the mycobacterial rpoB sequence includes at least about 5 bases of the mycobacterial rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 which differ from the corresponding at least about 5 bases in SEQ ID NO: 1 when the sequences are maximally aligned; wherein said stringent hybridization conditions comprise 5 x SSPE and a temperature of 25-30°C.

12. (Previously Amended) The polynucleotide of claim 11 that is a probe.

13. (Previously Amended) The polynucleotide of claim 12, wherein a central position of the probe aligns with the one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

14. (Previously Amended) The sequence-specific polynucleotide of claim 11 that is a primer.

15. (Previously Amended) The polynucleotide of claim 14, wherein the 3' end of the primer aligns with the one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

16. (Presently Amended) The polynucleotide of claim 11 that hybridizes under stringent hybridization conditions to at least 100 contiguous bases of a mycobacterial rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 or its **complement without hybridizing to the *M. tuberculosis* sequence of SEQ ID NO:1 or its complement.**